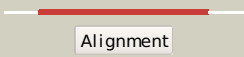
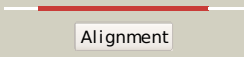
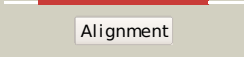
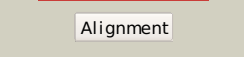
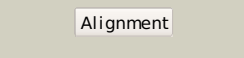
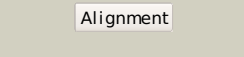
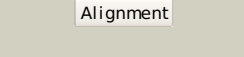
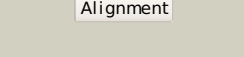
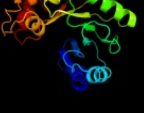
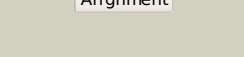
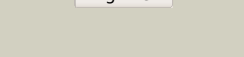


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                    |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">d1dxea</a>  |  Alignment   |    | 100.0      | 100    | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Hpch/Hpal aldolase                                                                                                                      |
| 2  | <a href="#">c2vwtA</a>  |  Alignment   |    | 100.0      | 43     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase;<br><b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex |
| 3  | <a href="#">c2v5jB</a>  |  Alignment   |    | 100.0      | 47     | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase;<br><b>PDBTitle:</b> apo class ii aldolase hpch                                                                                       |
| 4  | <a href="#">clizcA</a>  |  Alignment   |   | 100.0      | 28     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> macrophomate synthase intermolecular diels-alderase;<br><b>PDBTitle:</b> crystal structure analysis of macrophomate synthase                                                          |
| 5  | <a href="#">d1izcA</a>  |  Alignment |  | 100.0      | 28     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Hpch/Hpal aldolase                                                                                                                      |
| 6  | <a href="#">c3qz6A</a>  |  Alignment |  | 100.0      | 30     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase;<br><b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2                                                          |
| 7  | <a href="#">c1sgjB</a>  |  Alignment |  | 100.0      | 22     | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> citrate lyase, beta subunit;<br><b>PDBTitle:</b> crystal structure of citrate lyase beta subunit                                                                                      |
| 8  | <a href="#">d1sgja</a>  |  Alignment |  | 100.0      | 22     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Hpch/Hpal aldolase                                                                                                                      |
| 9  | <a href="#">d1u5ha</a>  |  Alignment |  | 100.0      | 22     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Hpch/Hpal aldolase                                                                                                                      |
| 10 | <a href="#">c1u5vA</a>  |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cite;<br><b>PDBTitle:</b> structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis                                                                 |
| 11 | <a href="#">d1e0ta2</a> |  Alignment |  | 100.0      | 17     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate kinase                                                                                                                         |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                                             |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c3qqwC_</a> | Alignment |    | 99.9 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative citrate lyase;<br><b>PDBTitle:</b> crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution                                                                   |
| 13 | <a href="#">c3qlIB_</a> | Alignment |    | 99.9 | 19 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> citrate lyase;<br><b>PDBTitle:</b> crystal structure of ripc from yersinia pestis                                                                                                                                         |
| 14 | <a href="#">c3r4iB_</a> | Alignment |    | 99.9 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> citrate lyase;<br><b>PDBTitle:</b> crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution                                                                             |
| 15 | <a href="#">d1liua2</a> | Alignment |    | 99.9 | 23 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate kinase                                                                                                                                                             |
| 16 | <a href="#">d1pkla2</a> | Alignment |    | 99.9 | 23 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate kinase                                                                                                                                                             |
| 17 | <a href="#">d1a3xa2</a> | Alignment |    | 99.9 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate kinase                                                                                                                                                             |
| 18 | <a href="#">d2q50a2</a> | Alignment |   | 99.9 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate kinase                                                                                                                                                             |
| 19 | <a href="#">c3pugA_</a> | Alignment |  | 99.8 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase;<br><b>PDBTitle:</b> haloferax volcanii malate synthase native at 3mm glyoxylate                                                                                                                    |
| 20 | <a href="#">c2hroA_</a> | Alignment |  | 99.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase;<br><b>PDBTitle:</b> structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus                                                           |
| 21 | <a href="#">c2hwgA_</a> | Alignment | not modelled                                                                        | 99.8 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase;<br><b>PDBTitle:</b> structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system                                                |
| 22 | <a href="#">c2bg5C_</a> | Alignment | not modelled                                                                        | 99.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phosphoenolpyruvate-protein kinase;<br><b>PDBTitle:</b> crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts) |
| 23 | <a href="#">c3cuzA_</a> | Alignment | not modelled                                                                        | 99.8 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase a;<br><b>PDBTitle:</b> atomic resolution structures of escherichia coli and2 bacillus anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design      |
| 24 | <a href="#">d1vbga1</a> | Alignment | not modelled                                                                        | 99.8 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain                                                                                                                              |
| 25 | <a href="#">d1h6za1</a> | Alignment | not modelled                                                                        | 99.8 | 20 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain                                                                                                                              |
| 26 | <a href="#">c3cuxA_</a> | Alignment | not modelled                                                                        | 99.8 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase;<br><b>PDBTitle:</b> atomic resolution structures of escherichia coli and2 bacillus anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design        |
| 27 | <a href="#">d1kbla1</a> | Alignment | not modelled                                                                        | 99.8 | 21 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain                                                                                                                              |
|    |                         |           |                                                                                     |      |    | <b>PDB header:</b> transferase                                                                                                                                                                                                                                                              |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                          |
|----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 28 | <a href="#">c1h6zA</a>  | Alignment | not modelled | 99.8 | 20 | <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase;<br><b>PDBTitle:</b> 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei                                                                             |
| 29 | <a href="#">c2olsA</a>  | Alignment | not modelled | 99.7 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate synthase;<br><b>PDBTitle:</b> the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis                                                         |
| 30 | <a href="#">c1kblA</a>  | Alignment | not modelled | 99.7 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase;<br><b>PDBTitle:</b> pyruvate phosphate dikinase                                                                                                                     |
| 31 | <a href="#">c1vbhA</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate,orthophosphate di kinase;<br><b>PDBTitle:</b> pyruvate phosphate dikinase with bound mg-pep from maize                                                                                  |
| 32 | <a href="#">c3khdC</a>  | Alignment | not modelled | 99.6 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure of pff1300w.                                                                                                                              |
| 33 | <a href="#">c3e0vB</a>  | Alignment | not modelled | 99.5 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions                                                                |
| 34 | <a href="#">c1t5aB</a>  | Alignment | not modelled | 99.5 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase, m2 isozyme;<br><b>PDBTitle:</b> human pyruvate kinase m2                                                                                                                        |
| 35 | <a href="#">c1pkIB</a>  | Alignment | not modelled | 99.5 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyruvate kinase);<br><b>PDBTitle:</b> the structure of leishmania pyruvate kinase                                                                                                       |
| 36 | <a href="#">c1e0tD</a>  | Alignment | not modelled | 99.5 | 21 | <b>PDB header:</b> phosphotransferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> r292d mutant of e. coli pyruvate kinase                                                                                                              |
| 37 | <a href="#">c2vgbB</a>  | Alignment | not modelled | 99.5 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase isozymes r/l;<br><b>PDBTitle:</b> human erythrocyte pyruvate kinase                                                                                                              |
| 38 | <a href="#">c1aqfB</a>  | Alignment | not modelled | 99.4 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate                                                                                       |
| 39 | <a href="#">c3t07D</a>  | Alignment | not modelled | 99.4 | 22 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid                             |
| 40 | <a href="#">c2e28A</a>  | Alignment | not modelled | 99.4 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus                                                                             |
| 41 | <a href="#">c1a3wB</a>  | Alignment | not modelled | 99.4 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+                                                                          |
| 42 | <a href="#">c3eoeC</a>  | Alignment | not modelled | 99.4 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007                                                                                      |
| 43 | <a href="#">c3ma8A</a>  | Alignment | not modelled | 99.3 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase;<br><b>PDBTitle:</b> crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum                                                                              |
| 44 | <a href="#">c3odmE</a>  | Alignment | not modelled | 98.4 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase;<br><b>PDBTitle:</b> archaeal-type phosphoenolpyruvate carboxylase                                                                                                     |
| 45 | <a href="#">d1qopa</a>  | Alignment | not modelled | 98.2 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                             |
| 46 | <a href="#">d1vhca</a>  | Alignment | not modelled | 98.2 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase                                                                                                                                                                    |
| 47 | <a href="#">d1rd5a</a>  | Alignment | not modelled | 98.2 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                             |
| 48 | <a href="#">d1rpxa</a>  | Alignment | not modelled | 98.1 | 11 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase                                                                                                                          |
| 49 | <a href="#">c3inpA</a>  | Alignment | not modelled | 98.0 | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase;<br><b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.                                |
| 50 | <a href="#">d2flia1</a> | Alignment | not modelled | 98.0 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase                                                                                                                          |
| 51 | <a href="#">c2qiWA</a>  | Alignment | not modelled | 98.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonmutase;<br><b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution |
| 52 | <a href="#">d1xi3a</a>  | Alignment | not modelled | 97.9 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Thiamin phosphate synthase<br><b>Family:</b> Thiamin phosphate synthase                                                                                                                                        |
| 53 | <a href="#">d1h1ya</a>  | Alignment | not modelled | 97.9 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase                                                                                                                          |
| 54 | <a href="#">c3eooL</a>  | Alignment | not modelled | 97.8 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase;<br><b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2                                                                                                    |

|    |                         |           |              |      |                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|--------------|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      | burkholderia pseudomallei                                                                                                                                                                                                                                     |
| 55 | <a href="#">d1xcfa_</a> | Alignment | not modelled | 97.8 | 17<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                           |
| 56 | <a href="#">c1zfjA_</a> | Alignment | not modelled | 97.8 | 20<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase;<br><b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes                              |
| 57 | <a href="#">c1zlpA_</a> | Alignment | not modelled | 97.8 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein;<br><b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct                                              |
| 58 | <a href="#">d1wbha1</a> | Alignment | not modelled | 97.8 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase                                                                                                                                                   |
| 59 | <a href="#">d1tqxa_</a> | Alignment | not modelled | 97.7 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase                                                                                                        |
| 60 | <a href="#">c2c3zA_</a> | Alignment | not modelled | 97.7 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus             |
| 61 | <a href="#">c3navB_</a> | Alignment | not modelled | 97.7 | 20<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961                  |
| 62 | <a href="#">c2hjpA_</a> | Alignment | not modelled | 97.7 | 18<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase;<br><b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++                                        |
| 63 | <a href="#">c2ekcA_</a> | Alignment | not modelled | 97.7 | 18<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5                                                                 |
| 64 | <a href="#">c3qc3B_</a> | Alignment | not modelled | 97.6 | 16<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase;<br><b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution             |
| 65 | <a href="#">c3igsB_</a> | Alignment | not modelled | 97.6 | 18<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2;<br><b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase                              |
| 66 | <a href="#">c1yadD_</a> | Alignment | not modelled | 97.5 | 18<br><b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni;<br><b>PDBTitle:</b> structure of teni from bacillus subtilis                                                                                         |
| 67 | <a href="#">d2tpsa_</a> | Alignment | not modelled | 97.5 | 13<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Thiamin phosphate synthase<br><b>Family:</b> Thiamin phosphate synthase                                                                                                                       |
| 68 | <a href="#">c3ih1A_</a> | Alignment | not modelled | 97.5 | 13<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase;<br><b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis                                            |
| 69 | <a href="#">c3ct7E_</a> | Alignment | not modelled | 97.5 | 17<br><b>PDB header:</b> isomerase<br><b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase;<br><b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12                                       |
| 70 | <a href="#">d1mxsa_</a> | Alignment | not modelled | 97.5 | 17<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase                                                                                                                                                   |
| 71 | <a href="#">c3b8iF_</a> | Alignment | not modelled | 97.5 | 21<br><b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase;<br><b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.        |
| 72 | <a href="#">d1muma_</a> | Alignment | not modelled | 97.4 | 14<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like                                                                                        |
| 73 | <a href="#">d1d8ca_</a> | Alignment | not modelled | 97.4 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Malate synthase G<br><b>Family:</b> Malate synthase G                                                                                                                                         |
| 74 | <a href="#">c3fa4D_</a> | Alignment | not modelled | 97.4 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase;<br><b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form                |
| 75 | <a href="#">c3o63B_</a> | Alignment | not modelled | 97.4 | 22<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable thiamine-phosphate pyrophosphorylase;<br><b>PDBTitle:</b> crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis                             |
| 76 | <a href="#">d1tqja_</a> | Alignment | not modelled | 97.4 | 12<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase                                                                                                        |
| 77 | <a href="#">c2ze3A_</a> | Alignment | not modelled | 97.3 | 21<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005;<br><b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus |
| 78 | <a href="#">c3qjaA_</a> | Alignment | not modelled | 97.3 | 21<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form                |
| 79 | <a href="#">d1wa3a1</a> | Alignment | not modelled | 97.2 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase                                                                                                                                                   |
|    |                         |           |              |      | <b>PDB header:</b> hydrolase                                                                                                                                                                                                                                  |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                               |
|-----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80  | <a href="#">c3lyeA_</a> | Alignment | not modelled | 97.2 | 12 | <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase;<br><b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase                                                                                                                                                                                                                    |
| 81  | <a href="#">dluiqa_</a> | Alignment | not modelled | 97.2 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like                                                                                                                                                                                              |
| 82  | <a href="#">dlyxya1</a> | Alignment | not modelled | 97.1 | 13 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> NanE-like                                                                                                                                                                                                                                       |
| 83  | <a href="#">dls2wa_</a> | Alignment | not modelled | 97.1 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like                                                                                                                                                                                              |
| 84  | <a href="#">dln8ia_</a> | Alignment | not modelled | 97.1 | 21 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Malate synthase G<br><b>Family:</b> Malate synthase G                                                                                                                                                                                                                                               |
| 85  | <a href="#">dljqna_</a> | Alignment | not modelled | 97.1 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Phosphoenolpyruvate carboxylase                                                                                                                                                                                                               |
| 86  | <a href="#">c3q58A_</a> | Alignment | not modelled | 96.9 | 17 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica                                                                                                                                       |
| 87  | <a href="#">dljqoa_</a> | Alignment | not modelled | 96.9 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Phosphoenolpyruvate carboxylase                                                                                                                                                                                                               |
| 88  | <a href="#">cljqoA_</a> | Alignment | not modelled | 96.9 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase;<br><b>PDBTitle:</b> crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize                                                                                                                                                               |
| 89  | <a href="#">c2v82A_</a> | Alignment | not modelled | 96.8 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br><b>PDBTitle:</b> kdpgal complexed to kdpgal                                                                                                                                                                                             |
| 90  | <a href="#">dli4na_</a> | Alignment | not modelled | 96.6 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                                                                                                 |
| 91  | <a href="#">dlvc4a_</a> | Alignment | not modelled | 96.6 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                                                                                                 |
| 92  | <a href="#">dlj5ta_</a> | Alignment | not modelled | 96.4 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                                                                                                 |
| 93  | <a href="#">dly0ea_</a> | Alignment | not modelled | 96.4 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> NanE-like                                                                                                                                                                                                                                       |
| 94  | <a href="#">d2p10a1</a> | Alignment | not modelled | 96.2 | 20 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> MII9387-like                                                                                                                                                                                                                                  |
| 95  | <a href="#">c2p10D_</a> | Alignment | not modelled | 96.2 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> mlI9387 protein;<br><b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution                                                                                                                     |
| 96  | <a href="#">dla53a_</a> | Alignment | not modelled | 95.9 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                                                                                                 |
| 97  | <a href="#">clpiiA_</a> | Alignment | not modelled | 95.8 | 15 | <b>PDB header:</b> bifunctional (isomerase and synthase)<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase;<br><b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution |
| 98  | <a href="#">dlzfja1</a> | Alignment | not modelled | 95.6 | 19 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH)<br><b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)                                                                                                                                                                                           |
| 99  | <a href="#">c3labA_</a> | Alignment | not modelled | 95.5 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpG (2-keto-3-deoxy-6-phosphogluconate)<br><b>PDBTitle:</b> crystal structure of a putative kdpG (2-keto-3-deoxy-6-2-phosphogluconate) aldolase from oleispira antarctica                                                                         |
| 100 | <a href="#">c3ez4B_</a> | Alignment | not modelled | 95.4 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase;<br><b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei                                                                                                           |
| 101 | <a href="#">c3cu2A_</a> | Alignment | not modelled | 94.9 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribulose-5-phosphate 3-epimerase;<br><b>PDBTitle:</b> crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution                                                                                                           |
| 102 | <a href="#">c2yw3E_</a> | Alignment | not modelled | 94.9 | 24 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1                                                                                                                                                                 |
| 103 | <a href="#">c2z6jB_</a> | Alignment | not modelled | 94.7 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acp reductase ii;<br><b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor                                                                                                                   |
| 104 | <a href="#">dlh5ya_</a> | Alignment | not modelled | 94.6 | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel                                                                                                                                                                                                                                                                   |

|     |                         |           |              |      |                                                                                                                                                                                                                                                                                      |
|-----|-------------------------|-----------|--------------|------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      | <b>Family:</b> Histidine biosynthesis enzymes                                                                                                                                                                                                                                        |
| 105 | <a href="#">d1w0ma_</a> | Alignment | not modelled | 94.6 | 18<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Triosephosphate isomerase (TIM)<br><b>Family:</b> Triosephosphate isomerase (TIM)                                                                                                                                    |
| 106 | <a href="#">d1mvoa_</a> | Alignment | not modelled | 94.5 | 14<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                   |
| 107 | <a href="#">d1dz3a_</a> | Alignment | not modelled | 94.5 | 12<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                   |
| 108 | <a href="#">c1znnF_</a> | Alignment | not modelled | 94.3 | 12<br><b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> plp synthase;<br><b>PDBTitle:</b> structure of the synthase subunit of plp synthase                                                                                                           |
| 109 | <a href="#">c3thaB_</a> | Alignment | not modelled | 94.1 | 23<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.                                                                                            |
| 110 | <a href="#">d1o4ua1</a> | Alignment | not modelled | 93.8 | 19<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like<br><b>Family:</b> NadC C-terminal domain-like                                                                                                                   |
| 111 | <a href="#">c3khjE_</a> | Alignment | not modelled | 93.7 | 19<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase;<br><b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64                                                                     |
| 112 | <a href="#">c3f4wA_</a> | Alignment | not modelled | 93.5 | 12<br><b>PDB header:</b> synthase, lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase;<br><b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium                                            |
| 113 | <a href="#">c1o4uA_</a> | Alignment | not modelled | 93.4 | 16<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolic acid phosphoribosyltransferase;<br><b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution            |
| 114 | <a href="#">d1a2oa1</a> | Alignment | not modelled | 93.2 | 17<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                   |
| 115 | <a href="#">d1q6oa_</a> | Alignment | not modelled | 93.0 | 9<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Decarboxylase                                                                                                                                                      |
| 116 | <a href="#">d1znnal</a> | Alignment | not modelled | 93.0 | 12<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> PdxS-like                                                                                                                                                         |
| 117 | <a href="#">d1ujpa_</a> | Alignment | not modelled | 92.9 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                   |
| 118 | <a href="#">d1oy0a_</a> | Alignment | not modelled | 92.9 | 16<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain<br><b>Family:</b> Ketopantoate hydroxymethyltransferase PanB                                                                                                                     |
| 119 | <a href="#">d1piia2</a> | Alignment | not modelled | 92.7 | 15<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                                   |
| 120 | <a href="#">c2bdqA_</a> | Alignment | not modelled | 92.5 | 17<br><b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc;<br><b>PDBTitle:</b> crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15. |